



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/509,449

Source: 1648

Date Processed by STIC: 2-22-01

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable-form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1648

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/509,449

DATE: 02/22/2001
 TIME: 12:05:50

Input Set : A:\ST25.txt
 Output Set: N:\CRF3\02222001\I509449.raw

Does Not Comply
 Corrected Diskette Needed

see p. 5

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3 <110> APPLICANT: Aoyagi, Katsumi
 4 Ohue, Chiharu
 5 Iida, Kumiko
 6 Yagi, Shintaro
 8 <120> TITLE OF INVENTION: Method for Measurement of Hepatitis C Virus
 10 <130> FILE REFERENCE: 594.352USWO
 12 <140> CURRENT APPLICATION NUMBER: 09/509,449
 13 <141> CURRENT FILING DATE: 2000-03-28
 15 <150> PRIOR APPLICATION NUMBER: JP-10-216094
 16 <151> PRIOR FILING DATE: 1998-07-30
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04129
 19 <151> PRIOR FILING DATE: 1999-07-30
 21 <160> NUMBER OF SEQ ID NOS: 12
 23 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 177
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Hepatitis C virus
 30 <400> SEQUENCE: 1
 32 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Pro Glu
 33 1 5 10 15
 35 Phe Met Gly Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr
 36 20 25 30
 38 Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
 39 35 40 45
 41 Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg
 42 50 55 60
 44 Ala Thr Arg Lys Thr Ser Lys Arg Ser Gln Pro Arg Gly Gly Arg Arg
 45 65 70 75 80
 47 Pro Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro
 48 85 90 95
 50 Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly
 51 100 105 110
 53 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp
 54 115 120 125
 56 Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr
 57 130 135 140
 59 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Phe Arg Val Gly Ala Phe
 60 145 150 155 160
 62 Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu
 63 165 170 175
 65 Asp
 68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 160
 70 <212> TYPE: PRT
 71 <213> ORGANISM: Hepatitis C virus
 73 <400> SEQUENCE: 2

RAW SEQUENCE LISTING DATE: 02/22/2001
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75 Met Gly Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
76 1          5          10          15
78 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
79          20          25          30
81 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
82          35          40          45
84 Thr Arg Lys Thr Ser Lys Arg Ser Gln Pro Arg Gly Gly Arg Arg Pro
85          50          55          60
87 Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly
88 65          70          75          80
90 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
91          85          90          95
93 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
94          100          105          110
96 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr Cys
97          115          120          125
99 Gly Phe Ala Asp Leu Met Gly Tyr Ile Phe Arg Val Gly Ala Phe Leu
100          130          135          140
102 Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
103 145          150          155          160
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 20
107 <212> TYPE: PRT
108 <213> ORGANISM: Artificial
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
113 <400> SEQUENCE: 3
115 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
116 1          5          10          15
118 Leu Pro Arg Arg
119          20
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 10
123 <212> TYPE: PRT
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
129 <400> SEQUENCE: 4
131 Gly Pro Arg Leu Gly Val Arg Ala Thr Arg
132 1          5          10
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 21
136 <212> TYPE: PRT
137 <213> ORGANISM: Artificial
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
142 <400> SEQUENCE: 5
144 Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg His Arg
145 1          5          10          15

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Input Set : A:\ST25.txt

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147 Ser Arg Asn Val Gly
148      20
150 <210> SEQ ID NO: 6
151 <211> LENGTH: 20
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
158 <400> SEQUENCE: 6
160 Asp Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
161 1      5      10      15
163 Thr Cys Gly Phe
164      20
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 24
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer for polymerase chain reaction.
174 <400> SEQUENCE: 7
175 gaattcatgg gcacgaatcc taaa
176      24
178 <210> SEQ ID NO: 8
179 <211> LENGTH: 21
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Primer for polymerase chain reaction.
186 <400> SEQUENCE: 8
187 ttagtctctcc agaaccgga c
188      21
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 16
192 <212> TYPE: PRT
193 <213> ORGANISM: Artificial
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Portion of Hepatitis C virus sequence.
198 <400> SEQUENCE: 9
200 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile
201 1      5      10      15
203 <210> SEQ ID NO: 10
204 <211> LENGTH: 1197
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Nucleotide sequence coding for chimeric antigen.
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (1)..(1188)
215 <400> SEQUENCE: 10
216 gaa ttc acc aaa gtg ccg gtt gct tat gcg gcc aaa ggt tat aag gtc
217      48

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217	Glu	Phe	Thr	Lys	Val	Pro	Val	Ala	Tyr	Ala	Ala	Lys	Gly	Tyr	Lys	Val	
218	1				5					10				15			
220	ctg	gtt	ctg	gac	ccg	agc	gtt	gcc	agc	acc	ctg	ggt	ttc	ggc	gcg	tat	96
221	Leu	Val	Leu	Asp	Pro	Ser	Val	Ala	Ser	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
222				20					25				30				
224	ctg	agc	aag	gcc	cat	ggt	gtg	aac	ccg	aac	atc	cgc	acg	ggc	atc	cgt	144
225	Leu	Ser	Lys	Ala	His	Gly	Val	Asn	Pro	Asn	Ile	Arg	Thr	Gly	Ile	Arg	
226			35					40				45					
228	acc	gtt	acc	acc	ggt	gct	ccg	gtg	acc	tat	tcc	acc	tac	ggt	aaa	tac	192
229	Thr	Val	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Tyr	
230		50					55					60					
232	ctg	gcg	gac	ggc	ggt	tgc	gcc	ggc	ggt	gcg	tac	gat	gtg	atc	gga	tct	240
233	Leu	Ala	Asp	Gly	Gly	Cys	Ala	Gly	Gly	Ala	Tyr	Asp	Val	Ile	Gly	Ser	
234	65					70				75					80		
236	gga	gag	gag	gtg	gcc	ctg	tct	aac	act	gga	gag	gtc	ccc	ttc	tat	gyc	288
237	Gly	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Val	Pro	Phe	Tyr	Gly	
238				85					90				95				
240	cgc	gcg	atc	ccg	atc	gaa	gcg	atc	aaa	ggc	ggt	cgc	cat	ctg	gtt	ttc	336
241	Arg	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Lys	Gly	Gly	Arg	His	Leu	Val	Phe	
242				100					105				110				
244	tgc	cat	agc	aag	gag	aaa	tgc	gat	gaa	ctg	gcg	agc	gcg	ctg	tcc	gga	384
245	Cys	His	Ser	Lys	Glu	Lys	Cys	Asp	Glu	Leu	Ala	Ser	Ala	Leu	Ser	Gly	
246			115					120				125					
248	ttg	ggt	ctg	aac	gct	gtg	gca	ttc	tat	cgc	ggt	ctg	gac	gtg	agc	att	432
249	Leu	Gly	Leu	Asn	Ala	Val	Ala	Phe	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Ile	
250		130				135					140						
252	atc	ccg	acc	cag	ggc	gat	gtg	gtt	atc	gtt	agc	acc	gat	gcg	ctg	atg	480
253	Ile	Pro	Thr	Gln	Gly	Asp	Val	Val	Ile	Val	Ser	Thr	Asp	Ala	Leu	Met	
254	145				150				155				160				
256	acc	ggt	ttt	acc	ggc	gat	ttt	gac	tca	gtg	gtc	gac	tgt	aac	aca	tgc	528
257	Thr	Gly	Phe	Thr	Gly	Asp	Phe	Asp	Ser	Val	Val	Asp	Cys	Asn	Thr	Cys	
258				165				170				175					
260	atc	acc	cag	gga	tct	gga	ctg	gta	agc	ttc	gcg	agc	cat	gtg	ccg	tac	576
261	Ile	Thr	Gln	Gly	Ser	Gly	Leu	Val	Ser	Phe	Ala	Ser	His	Val	Pro	Tyr	
262			180					185				190					
264	atc	gag	cag	ggt	atg	caa	ctg	agc	gaa	caa	ttt	aag	cag	aag	agc	ctg	624
265	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ser	Glu	Gln	Phe	Lys	Gln	Lys	Ser	Leu	
266			195				200					205					
268	ggt	ctg	ctg	cag	acc	gcg	acc	aaa	cag	gcg	gag	gcg	gcc	gcc	ccg	gtg	672
269	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	Ala	Ala	Pro	Val	
270		210				215					220						
272	gtt	ggc	acc	ccg	aaa	agc	cgc	cgt	ccg	gaa	ggt	cgt	gcc	tggt	gcg	caa	720
273	Val	Gly	Thr	Pro	Lys	Ser	Arg	Arg	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	
274	225				230					235					240		
276	ccg	ggt	acc	atc	atc	ctg	agc	ggt	cgt	ccg	gcg	gtt	gta	ccg	gat	cgt	768
277	Pro	Gly	Thr	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Val	Val	Pro	Asp	Arg	
278			245					250				255					
280	gaa	gtg	ctg	tat	caa	gaa	ttt	ctc	gag	gcc	tct	aga	gcg	gct	ctc	att	816
281	Glu	Val	Leu	Tyr	Gln	Glu	Phe	Leu	Glu	Ala	Ser	Arg	Ala	Ala	Leu	Ile	

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PATENT APPLICATION: US/09/509,449

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Input Set : A:\ST25.txt

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```

282          260          265          270
284 gaa gag ggg caa cgg ata gcc gag atg ctg aag tcc aag atc cag ggc      864
285 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
286          275          280          285
288 tta ctg cag caa gcc tcc aag cag gcc caa gac ata aaa atc gac ggt      912
289 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
290          290          295          300
292 acc ctg att att ccg aaa gat cgt cgc agc acc ggt aaa agc tgg ggt      960
293 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
294 305          310          315          320
296 aaa ccg ggc ttc ctg atc gat agc ttg cat atc aac cag cga gcc gtc      1008
297 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
298          325          330          335
300 gtt gca ccg gac aag gag gtc ctt tat gag gct ttt gat gag atg gag      1056
301 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
302          340          345          350
304 ctg gcc atg ggc acc aac ccg aaa ccg gag cgt aaa agc aag cgt aac      1104
305 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
306          355          360          365
308 acc aac cgt aaa ccg caa gat att aaa ttc ccg ggt agt ggt cag gtg      1152
309 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
310          370          375          380
312 gtg ggt ggt gtg tac ctg gtg ccg cgt cgt ggt ccg taaggatcc      1197
313 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
314 385          390          395
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 396
319 <212> TYPE: PRT
320 <213> ORGANISM: Artificial
322 <400> SEQUENCE: 11
324 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
325 1          5          10          15
328 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
329          20          25          30
332 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
333          35          40          45
336 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
337          50          55          60
340 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
341 65          70          75          80
344 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
345          85          90          95
348 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
349          100          105          110
352 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
353          115          120          125
356 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser -Ile
357          130          135          140
360 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met

```

Missing mandatory <220>, <223>
features to explain the source
of the artificial
sequence.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/509,449

DATE: 02/22/2001
TIME: 12:05:51

Input Set : A:\ST25.txt
Output Set: N:\CRF3\02222001\I509449.raw